

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.

(ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: Corporate Intellectual Property, UW2220.- 709
Swedeland Rd.
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/117,366
(B) FILING DATE: 07-SEP-1993
(C) CLASSIFICATION:

(A) APPLICATION NUMBER: US 08/136,783
(B) FILING DATE: 14-OCT-1993
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sutton, Jeffrey A.

45

GAA ATC AAA CGG
Glu Ile Lys Arg
130

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA 60

GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA 108
Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala
1 5 10 15

TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG 156
Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
20 25 30

CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA 204
Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
35 40 45

CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA 252
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
50 55 60

AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC 300
Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
65 70 75

TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC 348
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
80 85 90 95

AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT 396
Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
100 105 110

GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC 444
Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
115 120 125

GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA 483
Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser

130

135

140

(2) INFORMATION FOR SEQ ID NO:4:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala Tyr
 1             5             10             15
Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 20             25             30
Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 35             40             45
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 50             55             60
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
 65             70             75             80
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser
 85             90             95
Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala
 100            105            110
Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp
 115            120            125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 130            135            140

```

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

1 5 10 15

Gly Ala Tyr Gly

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs.
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
GTC CAC TCC	57
Val His Ser	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT	48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
GGT GCC TAC GGG CAG GTT ACC CTG AAA GAG TCT GGC CCT GGG ATA TTG	96
Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu	
20 25 30	
CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA	144
Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser	
35 40 45	
CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA	192
Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly	
50 55 60	

[illegible]

(1) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15
Gly Ala Tyr Gly Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
20 25 30

Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
 35 40 45
 Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
 50 55 60
 Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
 65 70 75 80
 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
 85 90 95
 Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
 100 105 110
 Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
 115 120 125
 Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 130 135 140

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GTG TTG CAG ACC CAG GTC TTC ATT TCT CTG TTG CTC TGG ATC TCT

48

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

GGT GCC TAC GGG CAG GTT ACC CTG CGT GAA TCC GGT CCG GCA CTA GTT 96
 Gly Ala Tyr Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val
 20 25 30

AAA CCG ACC CAG ACC CTG ACG TTA ACC TGC ACC TTC TCC GGT TTC TCC 144
 Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser
 35 40 45

CTG TCG ACC TCC GGT ATG GGT GTT TCC TGG ATC CGT CAG CCG CCG GGT 192
 Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly
 50 55 60

AAA GGT CTA GAA TGG CTG GCT CAC ATC TAC TGG GAC GAC GAC AAA CGT 240
 Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
 65 70 75 80

TAC AAC CCG AGC CTG AAA TCC CGT CTG ACG ATA TCC AAA GAC ACC TCC 288
 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
 85 90 95

CGT AAC CAG GTT GTT CTG ACC ATG ACT AAC ATG GAC CCG GTT GAC ACC 336
 Arg Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr
 100 105 110

GCT ACC TAC TAC TGC GCT CGA CGC GAA ACC GTT TTC TAC TGG TAC TTC 384
 Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
 115 120 125

GAC GTT TGG GGT CGT GGT ACC CCA GTT ACC GTG AGC TCA 423
 Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser
 130 135 140

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

Gly Ala Tyr Gly Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val
 20 25 30

Lys Pro Thr Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser
 35 40 45

Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly
 50 55 60

Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
 65 70 75 80

Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
 85 90 95

Arg Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr
 100 105 110

Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
 115 120 125

Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser
 130 135 140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
GTC CAC TCC GAT ATC GTG ATG ACC CAG TCT CCA GAC TCG CTA GCT GTG	96
Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val	
20 25 30	
TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC AAG GCC TCC CAA AGT GTT	144
Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val	
35 40 45	
GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAG CAG AAA CCC GGG	192
Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly	
50 55 60	
CAG CCT CCT AAG TTG CTC ATT TAC GCT GCA TCC AAT CTA GAA TCT GGG	240
Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly	
65 70 75 80	
GTA CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT CTC	288
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu	
85 90 95	
ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTA TAC TAC TGT CAG	336
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln	

(2) INFORMATION FOR SEQ ID NO:14:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

52

[illegible]

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 85 90 95

Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
 100 105 110

Gln Ser Asn Glu Asp Pro Pro Arg Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125

Ile Lys Arg
 130

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAG GCC AGC CAA AGT GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC 45
 Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(11) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

(A) NAME/KEY: CDS
(B) LOCATION: 1..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCT GCA TCC AAT CTA GAA TCT
Ala Ala Ser Asn Leu Glu Ser
1 5

21

(2) INFORMATION FOR SEQ ID NO:18:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Ser Asn Leu Glu Ser

1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAG CAA AGT AAT GAG GAT CCT CCG ACG

27

Gln Gln Ser Asn Glu Asp Pro Pro Thr

1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Gln Gln Ser Asn Glu Asp Pro Pro Thr
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..21

ACT TCT GGT ATG GGT GTG AGC
Thr Ser Gly Met Gly Val Ser
1 5

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Thr Ser Gly Met Gly Val Ser
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..48

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAC	ATT	TAC	TGG	GAT	GAT	GAC	AAG	CGC	TAT	AAC	CCA	TCC	CTG	AAG	AGC	48
His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	Tyr	Asn	Pro	Ser	Leu	Lys	Ser	
1			5				10						15			

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His	Ile	Tyr	Trp	Asp	Asp	Asp	Lys	Arg	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1			5				10						15		

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGA GAG ACT GTG TTC TAC TGG TAC TTC GAT GTC
 Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val
 1 5 10

33

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp Val
 1 5 10

58

Sequence

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAACTCA TTCCTGTTGA AGCTCTGAC AATGGG

36

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTACATATGC AAGGCTTACA ACCACAATC

29

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTTACCTG CGTGAATCCG GTCCGGCACT AGTTAAACCG ACCCAGACCC TGACGTTAAC 60
CTGCACCTTC TCCGGTTTCT CCCTGTCGAC CTCCGGTATG GGTGTTTCCT GGATCCG 117

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCAGCCGCCG GGTAAAGGTC TAGAATGGCT GGCTCACATC TACTGGGACG ACGACAAACG 60
TTACAACCCG AGCCTGAAAT CCCGTCTGAC GATATCCAAA GACACCTCCC GTAACCAGGT 120

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTTCTGACC ATGGACCCGG TTGACACCGC TACCTACTAC TGCCTCGTC GCGAAACCGT 60
TTTCTACTGG TACTTCGACG TTTGGGGTCG TGGTACCCCA GTTACCGTGA GCTCCCAACC 120

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCCGGCGGC TGACGGATCC AGGAA 25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGTCAGAA CAACCTGGTT ACGG 24

25

CCAACCCTCG AGTGCCATTG A

21

(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTAGCTGTGT CTCTGGGCGA GAGGGCCACC ATCAACTGCA AGG

43

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTTGCAGTT GATGGTGGCC CTCTGCCCCA GAGACACAG

39

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCGAGAGGCC TCCCAAAGTG TTGATTATGA TGGTGATAGT TATATGAACT GGTATCAGCA

60

GAAACCC

67

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGTTTCTGC TGATACCACT TCATATAACT ATCACCATCA TAATCAACAC TTTGGGAGGC 60
CTC 63

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATACTACTGT CAGCAAAGTA ATGAGGATCC TCCGAGGTTC GCGGAGGGA C 51

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGTCCCT CCGCCGAACC TCGGAGGATC CTCATTACTT TGCTGACAGT AGT

53

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(11) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGCAGCCTC CTAAGTTGCT CATTACGCT GCATCCAATC TAGAATCTGG GGTAC

55

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(1i) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCAGATTCT AGATTGGATG CAGCGTAAAT GAGCAACTTA GGAGGCTGCC C

51

(2) INFORMATION FOR SEQ ID NO:46:

Questions **A**nswers
The **S**chool **E**xchange
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is **a** **p**rogram **t**hat
gives **y**ou **a** **c**hoice
between **U.S.** dollars
and **foreign** currencies.
If **you** **are** **interested**
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(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AATTCGAGGA CGCCAGCAAC ATGGTGTTC AGACCCAGGT CTTCAATTCT CTGTTGCTCT 60
GGATCTCTGG TGCCTACGGG CAG 83

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTAACCTGCC CGTAGGCACC AGAGATCCAG AGCAACAGAG AAATGAAGAC CTGGGTCTGC 60
AACACCATGT TGCTGGCGTC CTCG 84

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGGTTACCC TGAAAGAGTC

20

(2) INFORMATION FOR SEQ ID NO:49:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(11) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAAGTAGTCC TTGACCAG

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACCGTCT CCTCAGCTAG CACCAAGGGG C

31

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(11) MOLECULE TYPE: DNA (genomic)

CTTGGTGCTA GCTGAGGAGA CG

22

(i) SEQUENCE CHARACTERISTICS:

(11) MOLECULE TYPE: DNA (genomic)

CATCTAGATG GCGCCGCCAC AGTACGTTTG ATCTCCAGCT TGGTCCC

47

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:53:

SECRET

AAGGCCTCCC AAAGTGTGA TTATGATGGT GATAGTTATA TGAAC

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACCTCCGGTA TGGGTGTTTC C

21

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACATCTACT GGGACGACGA CAAACGTTAC AACCCGAGCC TGAAATCC

48

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGCGAAACCG TTTTCTACTG GTACTTCGAC GTT

33

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	
GTC CAC TCC GAT ATC GTG ATG ACC CAG TCT CCA GAC TCG CTA GCT GTG	96
Val His Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val	
20 25 30	
TCT CTG GGC GAG AGG GCC ACC ATC AAC TGC AAG GCC TCC CAA AGT GTT	144
Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val	
35 40 45	

GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAT CAG CAG AAA CCC GGG 192
 Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly
 50 55 60

CAG CCT CCT AAG TTG CTC ATT TAC GCT GCA TCC AAT CTA GAA TCT GGG 240
 Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly
 65 70 75 80

GTA CCT GAC CGA TTC AGT GGC AGC GGG TCT GGG ACA GAT TTC ACT CTC 288
 Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 85 90 95

ACC ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTA TAC TAC TGT CAG 336
 Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
 100 105 110

CAA AGT AAT GAG GAT CCT CCG ACG TTC GGC GGA GGG ACC AAA GTG GAG 384
 Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu
 115 120 125

ATC AAA CGT 393
 Ile Lys Arg
 130

(2) INFORMATION FOR SEQ ID NO:58:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

[illegible]